OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/015,540

DATE: 03/21/2002
TIME: 11:10:40

Input Set : **A:\405c3.app**
Output Set: **N:\CRF3\03212002\J015540.raw**

SEQUENCE LISTING

```
 5 (1) GENERAL INFORMATION:
 7       (i) APPLICANT: Ling, Nicholas
 8                      Gaur, Amitabh
 9                      Conlon, Paul J.
10                      Steinman, Lawrence
13      (ii) TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE
14                      SCLEROSIS USING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC
15                      PROTEIN
17     (iii) NUMBER OF SEQUENCES: 3
19      (iv) CORRESPONDENCE ADDRESS:
20          (A) ADDRESSEE: Seed Intellectual Property Law Group PLLC
21          (B) STREET: 701 Fifth Avenue, Suite 6300
22          (C) CITY: Seattle
23          (D) STATE: Washington
24          (E) COUNTRY: USA
25          (F) ZIP: 98104-7092
27       (v) COMPUTER READABLE FORM:
28          (A) MEDIUM TYPE: Floppy disk
29          (B) COMPUTER: IBM PC compatible
30          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
31          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
33      (vi) CURRENT APPLICATION DATA:
C--> 34          (A) APPLICATION NUMBER: US/10/015,540
C--> 35          (B) FILING DATE: 11-Dec-2001
36          (C) CLASSIFICATION.
38    (vii) ATTORNEY/AGENT INFORMATION:
39          (A) NAME: Christiansen, William T.
40          (B) REGISTRATION NUMBER: 44,614
41          (C) REFERENCE/DOCKET NUMBER: 690068.405C3
43      (ix) TELECOMMUNICATION INFORMATION:
44          (A) TELEPHONE: (206) 622-4900
45          (B) TELEFAX: (206) 682-6031
48 (2) INFORMATION FOR SEQ ID NO: 1
50       (i) SEQUENCE CHARACTERISTICS:



         (ii) FEATURE:
              (A) NAME/KEY: CDS
60            (B) LOCATION: 1..510
```

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```
65 GCG TCA CAG AAG AGA CCC TCC CAG AGG CAC GGA TCC AAG TAC CTG GCC          48
66 Ala Ser Gln Lys Arg Pro Ser Gln Arg His Gly Ser Lys Tyr Leu Ala
67  1               5                   10                  15
69 ACA GCA AGT ACC ATG GAC CAT GCC AGG CAT GGC TTC CTC CCA AGG CAC          96
70 Thr Ala Ser Thr Met Asp His Ala Arg His Gly Phe Leu Pro Arg His
71          20                  25                  30
73 AGA GAC ACG GGC ATC CTT GAC TCC ATC GGG CGC TTC TTT GGC GGT GAC         144
74 Arg Asp Thr Gly Ile Leu Asp Ser Ile Gly Arg Phe Phe Gly Gly Asp
75          35                  40                  45
77 AGG GGT GCG CCA AAG CGG GGC TCT GGC AAG GAC TCA CAC CAC CCG GCA         192
78 Arg Gly Ala Pro Lys Arg Gly Ser Gly Lys Asp Ser His His Pro Ala
79          50                  55                  60
81 AGA ACT GCT CAC TAT GGC TCC CTG CCC CAG AAG TCA CAC GGC CGG ACC         240
82 Arg Thr Ala His Tyr Gly Ser Leu Pro Gln Lys Ser His Gly Arg Thr
83  65                  70                  75                  80
85 CAA GAT GAA AAC CCC GTA GTC CAC TTC TTC AAG AAC ATT GTG ACG CCT         288
86 Gln Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro
87                  85                  90                  95
89 CGC ACA CCA CCC CCG TCG CAG GGA AAG GGG AGA GGA CTG TCC CTG AGC         336
90 Arg Thr Pro Pro Pro Ser Gln Gly Lys Gly Arg Gly Leu Ser Leu Ser
91              100                 105                 110
93 AGA TTT AGC TGG GGG GCC GAA GGC CAG AGA CCA GGA TTT GGC TAC GGA         384
94 Arg Phe Ser Trp Gly Ala Glu Gly Gln Arg Pro Gly Phe Gly Tyr Gly
95              115                 120                 125
97 GGC AGA GCG TCC GAC TAT AAA TCG GCT CAC AAG GGA TTC AAG GGA GTC         432
98 Gly Arg Ala Ser Asp Tyr Lys Ser Ala His Lys Gly Phe Lys Gly Val
99          130                 135                 140
101 GAT GCC CAG GGC ACG CTT TCC AAA ATT TTT AAG CTG GGA GGA AGA GAT        480
102 Asp Ala Gln Gly Thr Leu Ser Lys Ile Phe Lys Leu Gly Gly Arg Asp
103 145                 150                 155                 160
105 AGT CGC TCT GGA TCA CCC ATG GCT AGA CGC TGA                            513
106 Ser Arg Ser Gly Ser Pro Met Ala Arg Arg
107              165                 170
110 (2) INFORMATION FOR SEQ ID NO: 2:
112      (i) SEQUENCE CHARACTERISTICS:
113          (A) LENGTH: 170 amino acids
114          (B) TYPE: amino acid
115          (D) TOPOLOGY: linear
117     (ii) MOLECULE TYPE: protein
119     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
121 Ala Ser Gln Lys Arg Pro Ser Gln Arg His Gly Ser Lys Tyr Leu Ala
122  1               5                   10                  15
124 Thr Ala Ser Thr Met Asp His Ala Arg His Gly Phe Leu Pro Arg His
125          20                  25                  30
```

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```
134  65                        70                  75                      80
136  Gln Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro
137               85                 90                  95
139  Arg Thr Pro Pro Pro Ser Gln Gly Lys Gly Arg Gly Leu Ser Leu Ser
140             100               105                 110
142  Arg Phe Ser Trp Gly Ala Glu Gly Gln Arg Pro Gly Phe Gly Tyr Gly
143          115               120                 125
145  Gly Arg Ala Ser Asp Tyr Lys Ser Ala His Lys Gly Phe Lys Gly Val
146      130               135                 140
148  Asp Ala Gln Gly Thr Leu Ser Lys Ile Phe Lys Leu Gly Gly Arg Asp
149  145               150                 155                     160
151  Ser Arg Ser Gly Ser Pro Met Ala Arg Arg
152             165                 170
154  (2) INFORMATION FOR SEQ ID NO: 3:
156     (i) SEQUENCE CHARACTERISTICS:
157          (A) LENGTH: 14 amino acids
158          (B) TYPE: amino acid
159          (C) STRANDEDNESS:
160          (D) TOPOLOGY: linear
166     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
168  Val Val His Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro
169  1               5                 10
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/015,540

DATE: 03/21/2002
TIME: 11:10:41

Input Set : **A:\405c3.app**
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L:34 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:35 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]